

Anthony J Wilkinson

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172
papers

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96
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179
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10,989
ext. citations

7.5
avg, IF

5.59
L-index

#	Paper	IF	Citations
172	Hydrogen bonding and biological specificity analysed by protein engineering. <i>Nature</i> , 1985 , 314, 235-8	50.4	1023
171	AAA+ superfamily ATPases: common structure--diverse function. <i>Genes To Cells</i> , 2001 , 6, 575-97	2.3	769
170	Condition-dependent transcriptome reveals high-level regulatory architecture in <i>Bacillus subtilis</i> . <i>Science</i> , 2012 , 335, 1103-6	33.3	602
169	The use of double mutants to detect structural changes in the active site of the tyrosyl-tRNA synthetase (<i>Bacillus stearothermophilus</i>). <i>Cell</i> , 1984 , 38, 835-40	56.2	538
168	Redesigning enzyme structure by site-directed mutagenesis: tyrosyl tRNA synthetase and ATP binding. <i>Nature</i> , 1982 , 299, 756-8	50.4	306
167	Site-directed mutagenesis as a probe of enzyme structure and catalysis: tyrosyl-tRNA synthetase cysteine-35 to glycine-35 mutation. <i>Biochemistry</i> , 1983 , 22, 3581-6	3.2	264
166	Global network reorganization during dynamic adaptations of <i>Bacillus subtilis</i> metabolism. <i>Science</i> , 2012 , 335, 1099-103	33.3	215
165	N-myristoyltransferase inhibitors as new leads to treat sleeping sickness. <i>Nature</i> , 2010 , 464, 728-32	50.4	213
164	Conserved arginine residues implicated in ATP hydrolysis, nucleotide-sensing, and inter-subunit interactions in AAA and AAA+ ATPases. <i>Journal of Structural Biology</i> , 2004 , 146, 106-12	3.4	202
163	Dissecting the role of a conserved motif (the second region of homology) in the AAA family of ATPases. Site-directed mutagenesis of the ATP-dependent protease FtsH. <i>Journal of Biological Chemistry</i> , 1999 , 274, 26225-32	5.4	165
162	Validation of N-myristoyltransferase as an antimalarial drug target using an integrated chemical biology approach. <i>Nature Chemistry</i> , 2014 , 6, 112-21	17.6	151
161	Global profiling of co- and post-translationally N-myristoylated proteomes in human cells. <i>Nature Communications</i> , 2014 , 5, 4919	17.4	148
160	Phosphorylated aspartate in the structure of a response regulator protein. <i>Journal of Molecular Biology</i> , 1999 , 294, 9-15	6.5	143
159	A large increase in enzyme-substrate affinity by protein engineering. <i>Nature</i> , 1984 , 307, 187-8	50.4	137
158	Structural factors governing heme dissociation from metmyoglobin. <i>Biochemistry</i> , 1996 , 35, 11300-9	3.2	133
157	Stability of myoglobin: a model for the folding of heme proteins. <i>Biochemistry</i> , 1994 , 33, 11767-75	3.2	129
156	The crystal structure of the AAA domain of the ATP-dependent protease FtsH of <i>Escherichia coli</i> at 1.5 Å resolution. <i>Structure</i> , 2002 , 10, 1073-83	5.2	110

155	The role of water in sequence-independent ligand binding by an oligopeptide transporter protein. <i>Nature Structural Biology</i> , 1996 , 3, 998-1001		103
154	The structure of the cofactor-binding fragment of the LysR family member, CysB: a familiar fold with a surprising subunit arrangement. <i>Structure</i> , 1997 , 5, 1017-32	5.2	101
153	Lipid spirals in <i>Bacillus subtilis</i> and their role in cell division. <i>Molecular Microbiology</i> , 2008 , 68, 1315-27	4.1	100
152	Protein engineering 20 years on. <i>Nature Reviews Molecular Cell Biology</i> , 2002 , 3, 964-70	48.7	99
151	Peptide binding in OppA, the crystal structures of the periplasmic oligopeptide binding protein in the unliganded form and in complex with lysyllysine. <i>Biochemistry</i> , 1997 , 36, 9747-58	3.2	90
150	An evolutionary link between sporulation and prophage induction in the structure of a repressor:anti-repressor complex. <i>Journal of Molecular Biology</i> , 1998 , 283, 907-12	6.5	87
149	Crystal structure of GerE, the ultimate transcriptional regulator of spore formation in <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2001 , 306, 759-71	6.5	86
148	The crystal structures of the oligopeptide-binding protein OppA complexed with tripeptide and tetrapeptide ligands. <i>Structure</i> , 1995 , 3, 1395-406	5.2	86
147	Distal pocket polarity in ligand binding to myoglobin: structural and functional characterization of a threonine68(E11) mutant. <i>Biochemistry</i> , 1991 , 30, 6252-60	3.2	86
146	The crystal structures of human S100A12 in apo form and in complex with zinc: new insights into S100A12 oligomerisation. <i>Journal of Molecular Biology</i> , 2009 , 391, 536-51	6.5	82
145	Probing histidine-substrate interactions in tyrosyl-tRNA synthetase using asparagine and glutamine replacements. <i>Biochemistry</i> , 1985 , 24, 5106-9	3.2	82
144	The structure of CodY, a GTP- and isoleucine-responsive regulator of stationary phase and virulence in gram-positive bacteria. <i>Journal of Biological Chemistry</i> , 2006 , 281, 11366-73	5.4	78
143	Serine92 (F7) contributes to the control of heme reactivity and stability in myoglobin. <i>Biochemistry</i> , 1993 , 32, 5132-8	3.2	78
142	Analysis of Enzyme Structure and Activity by Protein Engineering. <i>Angewandte Chemie International Edition in English</i> , 1984 , 23, 467-473		77
141	dUTPase as a platform for antimalarial drug design: structural basis for the selectivity of a class of nucleoside inhibitors. <i>Structure</i> , 2005 , 13, 329-38	5.2	75
140	N-myristoyltransferase from <i>Leishmania donovani</i> : structural and functional characterisation of a potential drug target for visceral leishmaniasis. <i>Journal of Molecular Biology</i> , 2010 , 396, 985-99	6.5	73
139	The crystal structure of gankyrin, an oncoprotein found in complexes with cyclin-dependent kinase 4, a 19 S proteasomal ATPase regulator, and the tumor suppressors Rb and p53. <i>Journal of Biological Chemistry</i> , 2004 , 279, 1541-5	5.4	71
138	Gankyrin: a new oncoprotein and regulator of pRb and p53. <i>Trends in Cell Biology</i> , 2006 , 16, 229-33	18.3	69

137	Contributions of residue 45(CD3) and heme-6-propionate to the biomolecular and geminate recombination reactions of myoglobin. <i>Biochemistry</i> , 1991 , 30, 4697-705	3.2	68
136	The substrate-binding protein in bacterial ABC transporters: dissecting roles in the evolution of substrate specificity. <i>Biochemical Society Transactions</i> , 2015 , 43, 1011-7	5.1	67
135	Distal pocket polarity in ligand binding to myoglobin: deoxy and carbonmonoxy forms of a threonine68(E11) mutant investigated by X-ray crystallography and infrared spectroscopy. <i>Biochemistry</i> , 1993 , 32, 13061-70	3.2	66
134	Dimer formation and transcription activation in the sporulation response regulator Spo0A. <i>Journal of Molecular Biology</i> , 2002 , 316, 235-45	6.5	64
133	An ATP-binding cassette-type cysteine transporter in <i>Campylobacter jejuni</i> inferred from the structure of an extracytoplasmic solute receptor protein. <i>Molecular Microbiology</i> , 2005 , 57, 143-55	4.1	63
132	Domain swapping in the sporulation response regulator Spo0A. <i>Journal of Molecular Biology</i> , 2000 , 297, 757-70	6.5	61
131	Conservation of structure and mechanism in primary and secondary transporters exemplified by SiaP, a sialic acid binding virulence factor from <i>Haemophilus influenzae</i> . <i>Journal of Biological Chemistry</i> , 2006 , 281, 22212-22222	5.4	60
130	Selective inhibitors of protozoan protein N-myristoyltransferases as starting points for tropical disease medicinal chemistry programs. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1625	4.8	58
129	Mechanism of hydrogen cyanide binding to myoglobin. <i>Biochemistry</i> , 1996 , 35, 7107-13	3.2	58
128	Alteration of axial coordination by protein engineering in myoglobin. Bisimidazole ligation in the His64-->Val/Val68-->His double mutant. <i>Journal of Biological Chemistry</i> , 1995 , 270, 15993-6001	5.4	55
127	Discovery of <i>Plasmodium vivax</i> N-myristoyltransferase inhibitors: screening, synthesis, and structural characterization of their binding mode. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 3578-82	8.3	54
126	The structure of the oligopeptide-binding protein, AppA, from <i>Bacillus subtilis</i> in complex with a nonapeptide. <i>Journal of Molecular Biology</i> , 2005 , 345, 879-92	6.5	54
125	Expression of HIV-1 gp120 and human soluble CD4 by recombinant baculoviruses and their interaction in vitro. <i>AIDS Research and Human Retroviruses</i> , 1990 , 6, 765-73	1.6	54
124	Fragment-derived inhibitors of human N-myristoyltransferase block capsid assembly and replication of the common cold virus. <i>Nature Chemistry</i> , 2018 , 10, 599-606	17.6	53
123	Design and synthesis of high affinity inhibitors of <i>Plasmodium falciparum</i> and <i>Plasmodium vivax</i> N-myristoyltransferases directed by ligand efficiency dependent lipophilicity (LELP). <i>Journal of Medicinal Chemistry</i> , 2014 , 57, 2773-88	8.3	52
122	pBaSysBioII: an integrative plasmid generating gfp transcriptional fusions for high-throughput analysis of gene expression in <i>Bacillus subtilis</i> . <i>Microbiology (United Kingdom)</i> , 2010 , 156, 1600-1608	2.9	52
121	A fluorescence-based assay for N-myristoyltransferase activity. <i>Analytical Biochemistry</i> , 2012 , 421, 342-43.1		51
120	Higher-throughput approaches to crystallization and crystal structure determination. <i>Biochemical Society Transactions</i> , 2008 , 36, 771-5	5.1	51

119	An $[\{Fe(mecam)\}_2]_6$ - bridge in the crystal structure of a ferric enterobactin binding protein. <i>Angewandte Chemie - International Edition</i> , 2006 , 45, 5132-6	16.4	50
118	Probing the mechanism of ATP hydrolysis and substrate translocation in the AAA protease FtsH by modelling and mutagenesis. <i>Molecular Microbiology</i> , 2001 , 39, 890-903	4.1	50
117	Division site recognition in Escherichia coli and Bacillus subtilis. <i>FEMS Microbiology Reviews</i> , 2007 , 31, 311-26	15.1	49
116	Crystal structure of dihydrodipicolinate synthase (BA3935) from Bacillus anthracis at 1.94 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 297-301	4.2	47
115	Discovery of novel and ligand-efficient inhibitors of Plasmodium falciparum and Plasmodium vivax N-myristoyltransferase. <i>Journal of Medicinal Chemistry</i> , 2013 , 56, 371-5	8.3	46
114	Residues in the distal heme pocket of neuroglobin. Implications for the multiple ligand binding steps. <i>Journal of Biological Chemistry</i> , 2004 , 279, 5886-93	5.4	46
113	Design and synthesis of inhibitors of Plasmodium falciparum N-myristoyltransferase, a promising target for antimalarial drug discovery. <i>Journal of Medicinal Chemistry</i> , 2012 , 55, 8879-90	8.3	45
112	Structure of components of an intercellular channel complex in sporulating Bacillus subtilis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 5441-5	11.5	45
111	The crystal structure of YloQ, a circularly permuted GTPase essential for Bacillus subtilis viability. <i>Journal of Molecular Biology</i> , 2004 , 340, 767-82	6.5	45
110	Structure-based design of potent and selective Leishmania N-myristoyltransferase inhibitors. <i>Journal of Medicinal Chemistry</i> , 2014 , 57, 8664-70	8.3	44
109	Structural and biochemical characterization of a mitochondrial peroxiredoxin from Plasmodium falciparum. <i>Molecular Microbiology</i> , 2006 , 61, 948-59	4.1	44
108	Tension in haemoglobin revealed by Fe-His(F8) bond rupture in the fully liganded T-state. <i>Journal of Molecular Biology</i> , 1997 , 271, 161-7	6.5	41
107	Structural basis of the sulphate starvation response in E. coli: crystal structure and mutational analysis of the cofactor-binding domain of the Cbl transcriptional regulator. <i>Journal of Molecular Biology</i> , 2006 , 364, 309-22	6.5	38
106	Interactions among residues CD3, E7, E10, and E11 in myoglobins: attempts to simulate the ligand-binding properties of Aplysia myoglobin. <i>Biochemistry</i> , 1995 , 34, 8715-25	3.2	38
105	Fine structure-activity analysis of mutations at position 51 of tyrosyl-tRNA synthetase. <i>Biochemistry</i> , 1985 , 24, 5858-61	3.2	38
104	Structure of the catalytic domain of the human mitochondrial Lon protease: proposed relation of oligomer formation and activity. <i>Protein Science</i> , 2010 , 19, 987-99	6.3	37
103	Genetic and biochemical analysis of the interaction of Bacillus subtilis CodY with branched-chain amino acids. <i>Journal of Bacteriology</i> , 2009 , 191, 6865-76	3.5	36
102	The trans-activation domain of the sporulation response regulator Spo0A revealed by X-ray crystallography. <i>Molecular Microbiology</i> , 2000 , 38, 198-212	4.1	36

101	Structure of the Bacillus cell fate determinant SpoIIAA in phosphorylated and unphosphorylated forms. <i>Structure</i> , 2001 , 9, 605-14	5.2	35
100	Crystallisation of the Bacillus subtilis sporulation inhibitor SinR, complexed with its antagonist, SinI. <i>FEBS Letters</i> , 1996 , 378, 98-100	3.8	33
99	Structural rearrangement accompanying ligand binding in the GAF domain of CodY from Bacillus subtilis. <i>Journal of Molecular Biology</i> , 2009 , 390, 1007-18	6.5	32
98	Oligomerization of the Bacillus subtilis division protein DivIVA. <i>Microbiology (United Kingdom)</i> , 2002 , 148, 807-813	2.9	32
97	Control of Initiation of DNA Replication in Bacillus subtilis and Escherichia coli. <i>Genes</i> , 2017 , 8,	4.2	31
96	Small subunits of RNA polymerase: localization, levels and implications for core enzyme composition. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 3532-3543	2.9	31
95	Stabilizing bound O2 in myoglobin by valine68 (E11) to asparagine substitution. <i>Biochemistry</i> , 1998 , 37, 15896-907	3.2	31
94	Reduction in CD4 binding affinity associated with removal of a single glycosylation site in the external glycoprotein of HIV-2. <i>Virology</i> , 1991 , 180, 853-6	3.6	31
93	Structural basis for the efficient phosphorylation of AZT-MP (3Razido-3Rdeoxythymidine monophosphate) and dGMP by Plasmodium falciparum type I thymidylate kinase. <i>Biochemical Journal</i> , 2010 , 428, 499-509	3.8	30
92	Crystallographic and solution studies of N-lithocholyl insulin: a new generation of prolonged-acting human insulins. <i>Biochemistry</i> , 2004 , 43, 5987-95	3.2	30
91	Analyse von Struktur-Aktivitäts-Beziehungen bei Enzymen durch Protein-Engineering. <i>Angewandte Chemie</i> , 1984 , 96, 455-462	3.6	30
90	Structure and organisation of SinR, the master regulator of biofilm formation in Bacillus subtilis. <i>Journal of Molecular Biology</i> , 2011 , 411, 597-613	6.5	29
89	The crystal structures of macrophage migration inhibitory factor from Plasmodium falciparum and Plasmodium berghei. <i>Protein Science</i> , 2009 , 18, 2578-91	6.3	29
88	A bacterial virulence factor with a dual role as an adhesin and a solute-binding protein: the crystal structure at 1.5 Å resolution of the PEB1a protein from the food-borne human pathogen Campylobacter jejuni. <i>Journal of Molecular Biology</i> , 2007 , 372, 160-71	6.5	28
87	High-resolution X-ray structures of pig metmyoglobin and two CD3 mutants: Mb(Lys45----Arg) and Mb(Lys45----Ser). <i>Biochemistry</i> , 1992 , 31, 8732-9	3.2	28
86	Diverse modes of binding in structures of Leishmania major N-myristoyltransferase with selective inhibitors. <i>IUCrJ</i> , 2014 , 1, 250-60	4.7	27
85	Changes of lipid domains in Bacillus subtilis cells with disrupted cell wall peptidoglycan. <i>FEMS Microbiology Letters</i> , 2011 , 325, 92-8	2.9	27
84	Where asymmetry in gene expression originates. <i>Molecular Microbiology</i> , 2005 , 57, 611-20	4.1	27

83	Structure and interactions of the Bacillus subtilis sporulation inhibitor of DNA replication, SirA, with domain I of DnaA. <i>Molecular Microbiology</i> , 2014 , 93, 975-91	4.1	25
82	Functional role for a conserved aspartate in the Spo0E signature motif involved in the dephosphorylation of the Bacillus subtilis sporulation regulator Spo0A. <i>Journal of Biological Chemistry</i> , 2008 , 283, 2962-72	5.4	25
81	Structure and non-essential function of glycerol kinase in Plasmodium falciparum blood stages. <i>Molecular Microbiology</i> , 2009 , 71, 533-45	4.1	24
80	Site-selective C-C modification of proteins at neutral pH using organocatalyst-mediated cross aldol ligations. <i>Chemical Science</i> , 2018 , 9, 5585-5593	9.4	24
79	Peptidomimetic inhibitors of N-myristoyltransferase from human malaria and leishmaniasis parasites. <i>Organic and Biomolecular Chemistry</i> , 2014 , 12, 8132-7	3.9	23
78	Structure of the phosphatase domain of the cell fate determinant SpoIIIE from Bacillus subtilis. <i>Journal of Molecular Biology</i> , 2012 , 415, 343-58	6.5	23
77	Compensating stereochemical changes allow murein tripeptide to be accommodated in a conventional peptide-binding protein. <i>Journal of Biological Chemistry</i> , 2011 , 286, 31512-21	5.4	23
76	Dimer-induced signal propagation in Spo0A. <i>Molecular Microbiology</i> , 2004 , 53, 829-42	4.1	23
75	Structures of Plasmodium falciparum purine nucleoside phosphorylase complexed with sulfate and its natural substrate inosine. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005 , 61, 1245-54		23
74	Application of high-throughput technologies to a structural proteomics-type analysis of Bacillus anthracis. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006 , 62, 1267-75		22
73	The crystal structure of superoxide dismutase from Plasmodium falciparum. <i>BMC Structural Biology</i> , 2006 , 6, 20	2.7	22
72	The response regulator Spo0A from Bacillus subtilis is efficiently phosphorylated in Escherichia coli. <i>FEMS Microbiology Letters</i> , 2003 , 223, 153-7	2.9	22
71	Apomyoglobin as a molecular recognition surface: expression, reconstitution and crystallization of recombinant porcine myoglobin in Escherichia coli. <i>Protein Engineering, Design and Selection</i> , 1988 , 2, 233-7	1.9	22
70	Structure of the Branched-chain Amino Acid and GTP-sensing Global Regulator, CodY, from. <i>Journal of Biological Chemistry</i> , 2017 , 292, 2714-2728	5.4	21
69	The Spore Coat Protein CotE Facilitates Host Colonization by Clostridium difficile. <i>Journal of Infectious Diseases</i> , 2017 , 216, 1452-1459	7	20
68	CRYSTAL STRUCTURES OF PERIPLASMIC SOLUTE-BINDING PROTEINS IN ABC TRANSPORT COMPLEXES ILLUMINATE THEIR FUNCTION 2003 , 187-207		20
67	Quaternary re-arrangement analysed by spectral enhancement: the interaction of a sporulation repressor with its antagonist. <i>Journal of Molecular Biology</i> , 1999 , 293, 997-1004	6.5	20
66	Discovery of high affinity inhibitors of -myristoyltransferase. <i>MedChemComm</i> , 2015 , 6, 1761-1766	5	18

65	Tetramerization and interdomain flexibility of the replication initiation controller YabA enables simultaneous binding to multiple partners. <i>Nucleic Acids Research</i> , 2016 , 44, 449-63	20.1	18
64	Mucosal Antibodies to the C Terminus of Toxin A Prevent Colonization of <i>Clostridium difficile</i> . <i>Infection and Immunity</i> , 2017 , 85,	3.7	17
63	The GTPase, CpgA(YloQ), a putative translation factor, is implicated in morphogenesis in <i>Bacillus subtilis</i> . <i>Molecular Genetics and Genomics</i> , 2006 , 275, 409-20	3.1	17
62	Crystallization of the GTP-dependent transcriptional regulator CodY from <i>Bacillus subtilis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 155-7		17
61	Engineering a ligand binding pocket into a four-helix bundle protein cytochrome b(562). <i>Journal of the American Chemical Society</i> , 2001 , 123, 512-3	16.4	16
60	An oscillating Min system in <i>Bacillus subtilis</i> influences asymmetrical septation during sporulation. <i>Microbiology (United Kingdom)</i> , 2012 , 158, 1972-1981	2.9	16
59	Cysteine thiolate coordination in the ferrous CO complex of an engineered cytochrome b562. <i>Journal of the American Chemical Society</i> , 2001 , 123, 2458-9	16.4	15
58	Raman and CD spectroscopy of recombinant 68-kDa DNA human topoisomerase I and its complex with suicide DNA-substrate. <i>Biochemistry</i> , 1998 , 37, 14630-42	3.2	14
57	Impact of CodY protein on metabolism, sporulation and virulence in <i>Clostridioides difficile</i> ribotype 027. <i>PLoS ONE</i> , 2019 , 14, e0206896	3.7	13
56	Structural characterization of Spo0E-like protein-aspartic acid phosphatases that regulate sporulation in bacilli. <i>Journal of Biological Chemistry</i> , 2006 , 281, 37993-8003	5.4	13
55	Inversion of axial coordination in myoglobin to create a "proximal" ligand binding pocket. <i>Biochemistry</i> , 2003 , 42, 10191-9	3.2	13
54	Structure of purine nucleoside phosphorylase (DeoD) from <i>Bacillus anthracis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005 , 61, 459-62		13
53	A new mutation in spo0A with intragenic suppressors in the effector domain. <i>FEMS Microbiology Letters</i> , 2000 , 185, 123-8	2.9	13
52	The structure and interactions of SpoIIISA and SpoIIISB, a toxin-antitoxin system in <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2011 , 286, 6808-19	5.4	12
51	A widespread family of serine/threonine protein phosphatases shares a common regulatory switch with proteasomal proteases. <i>ELife</i> , 2017 , 6,	8.9	12
50	Structure of the virulence-associated protein VapD from the intracellular pathogen <i>Rhodococcus equi</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 2139-51		11
49	Crystal structure of PurE (BA0288) from <i>Bacillus anthracis</i> at 1.8 Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 61, 674-6	4.2	11
48	Crystallization of the periplasmic oligopeptide-binding protein of <i>Salmonella typhimurium</i> . <i>Journal of Molecular Biology</i> , 1988 , 204, 493-4	6.5	11

47	Discovery of pyridyl-based inhibitors of -myristoyltransferase. <i>MedChemComm</i> , 2015 , 6, 1767-1772	5	10
46	Structural characterisation of the virulence-associated protein VapG from the horse pathogen <i>Rhodococcus equi</i> . <i>Veterinary Microbiology</i> , 2015 , 179, 42-52	3.3	10
45	Expression of soluble, active fragments of the morphogenetic protein SpoIIE from <i>Bacillus subtilis</i> using a library-based construct screen. <i>Protein Engineering, Design and Selection</i> , 2010 , 23, 817-25	1.9	10
44	Accommodating structurally diverse peptides in proteins. <i>Chemistry and Biology</i> , 1996 , 3, 519-24		10
43	The <i>Rhodococcus equi</i> virulence protein VapA disrupts endolysosome function and stimulates lysosome biogenesis. <i>MicrobiologyOpen</i> , 2017 , 6, e00416	3.4	9
42	Crystallization of gankyrin, an oncoprotein that interacts with CDK4 and the S6b (rpt3) ATPase of the 19S regulator of the 26S proteasome. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1294-5		9
41	Structure-guided optimization of quinoline inhibitors of -myristoyltransferase. <i>MedChemComm</i> , 2017 , 8, 191-197	5	8
40	Crystal and solution studies reveal that the transcriptional regulator AcnR of <i>Corynebacterium glutamicum</i> is regulated by citrate-Mg ²⁺ binding to a non-canonical pocket. <i>Journal of Biological Chemistry</i> , 2013 , 288, 15800-12	5.4	8
39	MpaA is a murein-tripeptide-specific zinc carboxypeptidase that functions as part of a catabolic pathway for peptidoglycan-derived peptides in ϵ proteobacteria. <i>Biochemical Journal</i> , 2012 , 448, 329-41	3.8	8
38	Morphogenic Protein RodZ Interacts with Sporulation Specific SpoIIE in <i>Bacillus subtilis</i> . <i>PLoS ONE</i> , 2016 , 11, e0159076	3.7	8
37	Crystallization and preliminary crystallographic studies of the cofactor-binding domain of the LysR-type transcriptional regulator Cbl from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1654-7		7
36	Structures of two superoxide dismutases from <i>Bacillus anthracis</i> reveal a novel active centre. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005 , 61, 621-4		7
35	Crystallization of full-length CysB of <i>Klebsiella aerogenes</i> , a LysR-type transcriptional regulator. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001 , 57, 260-2		7
34	Solution of the structure of the cofactor-binding fragment of CysB: a struggle against non-isomorphism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 369-78		7
33	Crystallization of the regulatory and effector domains of the key sporulation response regulator Spo0A. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999 , 55, 671-6		7
32	Crystal structure of the putative peptide-binding protein AppA from <i>Clostridium difficile</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019 , 75, 246-253	1.1	6
31	Structure mediation in substrate binding and post-translational processing of penicillin acylases: Information from mutant structures of <i>Kluyvera citrophila</i> penicillin G acylase. <i>Protein Science</i> , 2015 , 24, 1660-70	6.3	6
30	Crystallization of the AAA domain of the ATP-dependent protease FtsH of <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 1066-7		6

29	Crystallization of a DNA and N-acetylserine binding fragment (residues 1 to 233) of <i>Klebsiella aerogenes</i> CysB protein, a member of the LysR family. <i>Journal of Molecular Biology</i> , 1994 , 235, 1159-61	6.5	6
28	<i>Leishmania</i> differentiation requires ubiquitin conjugation mediated by a UBC2-UEV1 E2 complex. <i>PLoS Pathogens</i> , 2020 , 16, e1008784	7.6	6
27	Novel Thienopyrimidine Inhibitors of γ -Myristoyltransferase with On-Target Activity in Intracellular Amastigotes. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 7740-7765	8.3	5
26	Cloning, overexpression, crystallization and preliminary X-ray crystallographic analysis of a slow-processing mutant of penicillin G acylase from <i>Kluyvera citrophila</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 925-9		5
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